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Sequence 1: ssa (448 residues)

Sequence 2: seq (448 residues)

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

76.6% identity in 445 residues overlap; Score: 1857.0; Gap frequency: 0.0%

seq 1 MNMPETGPAGIASQLKLDHWMFYTANRNFORDPRLIVAAEGNYLVDDHGRKIFDALSGL
seq 1 MNQPLNVAPPVSSSELNLRHWMFFSANRNFQKDPRIIVAAEGSWLTDGKRKYVDSLGL

```
seq 61 WTCGAGHTRKEIADAVTRQLSTLDYSPAFQFGHPLSFQLAEKIAELVPGNLNHVFTNSG
seq 61 WTCGAGHSRKEIQEAVARQLGTLTDYSPGFQYGHPLSFQLAEKIAGLLPGELNHVFFTGSG
***** **
```

```
seq 121 SECADTALKMVRAYWRLKGQATKTKIIGRARGYHGVNIAGTSLGGVNGNRKMFQGQLLDVD
seq 121 SECADTSIKMARAYWRLKGQPKTKLIGRARGYHGVNVAGTSLGGIGGNRKMFQQLMDVD
*****
```

```
seq      181 HLPHTVLPVNAFSKGLPEEGGIALADEMLKLIELHDASNIAAVIVEPLAGSAGVLPFPKG
seq      181 HLPHTLQPGMAFTRGMAQTGGVELANELKLIELHDASNIAAVIVEPMMSGAGVLPFPVG
          * * * * *
```

```
seq      241 YLKRLREICTQHNILLIFDEVITGFGRMGAMTGSEAFGVTPDLMCIAKQVNTGAIPMGAV
seq      241 YLQRLREICDQHNNILLIFDEVITATGRLGTYSGAEYFVGVTPLMNVAKQVNTGAVPMGAV
          * * * * *
```

seq 301 IASSEIYQTFMNQPTPEYAVEFFHGYTSAHPVACAAGLAALDLOKENLYQSAELAPH
seq 301 IASSEIYDTFMNQALPEHAVEFHHGYTSAHPVACAAGLAALDILARDNLYQSAELAPH

```

*****
seq      361 FEKLLHGVKGTKNIVDIRNYGLAGAIQIAARDGDAIVRPYEAMKLWKAGFYVRFGGDTL
seq      361 FEKGLHGLQGAKNVIDIRNCGLAGAIQIAPRDGDPTVRPFEAGMKLWQQGFYVRFGGDTL
          * * * * *
seq      421 QFGPTENTKPOELDRLFDVGETLN
seq      421 QFGPTENARPEELDRLFDVGEALN
          * * * * *

```

32.0% identity in 25 residues overlap; Score: 29.0; Gap frequency: 0.0%

```

seq      315 TPEYAVEFPHGYTYSAPVACAAGL
seq      82  TLDYSPGFQYGHPLSFQLAEKIAGL
          * * * * *

```

23.1% identity in 26 residues overlap; Score: 27.0; Gap frequency: 0.0%

```

seq      211 LIELHDASNIAAVIVEPLAGSAGVLP
seq      374 VIDIRNCGLAGAIQIAPRDGDPTVRP
          * * * * *

```

33.3% identity in 15 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      120 GSECADTALKMVRAY
seq      201 GVELANELLKIELH
          * * * *

```

25.0% identity in 28 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      82  TLDYSPATQFGHPLSFQLAEKIAELVPG
seq      419 TLQFGPTFNARPEELDRLFDVGEALNG
          * * * *

```

36.4% identity in 11 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      400 YEAMKLWKAG
seq      54  YDSLGLWTCG
          * * *

```

38.5% identity in 13 residues overlap; Score: 26.0; Gap frequency: 0.0%

```

seq      3  MPETGPAGIASQL
seq      196 MAQTGGVELANEL
          * * *

```

27.3% identity in 22 residues overlap; Score: 25.0; Gap frequency: 0.0%

```

seq      253 WILLIFDEVITCFGRMGAMTGS
seq      282 DLMNVAKQVTNGAVPMGAVIAS

```

30.4% identity in 23 residues overlap; Score: 25.0; Gap frequency: 0.0%

seq 242 LKRLREICTQHNILLIFDEVITG
seq 208 LLKLIELHDASNIAAVIVEPMSG
* * * * *

50.0% identity in 10 residues overlap; Score: 25.0; Gap frequency: 0.0%

seq 99 LAEKIAELVP
seq 350 LVQQSAGELAP
* * * *

30.4% identity in 23 residues overlap; Score: 25.0; Gap frequency: 0.0%

seq 214 LHDASNIAAVIVEPLAGSAGVLP
seq 368 LOGARNVIDIRNCGLAGAIQIAP
* * * * *

50.0% identity in 8 residues overlap; Score: 24.0; Gap frequency: 0.0%

seq 4 PETGPAGI
seq 227 PMSGGAGV
* * *

62.5% identity in 8 residues overlap; Score: 24.0; Gap frequency: 0.0%

seq 385 AIQIAARD
seq 341 ALDILARD
* * *

23.3% identity in 30 residues overlap; Score: 24.0; Gap frequency: 0.0%

seq 63 CGAGHTRKEIADAVTRQLSTLDYSAPFQEG
seq 335 CAAGLAALDILARDNLVQQSAGELAPHFEKG
* * * * *

35.3% identity in 17 residues overlap; Score: 24.0; Gap frequency: 0.0%

seq 210 KLIELHDASNIAAVIVE
seq 244 RLREICDOHNILLIFDE
* * * * *

50.0% identity in 8 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 325 GYTYSANP
seq 423 GPTFNARP
* * * *

100.0% identity in 4 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 311 MNQP
seq 1 MNQP

45.5% identity in 11 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 218 SNIAAVIVEPL
seq 229 SGSAGVLVPPV
* * * *

50.0% identity in 8 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 419 TLQFGPTF
seq 82 TLDYSPGF
* * * *

60.0% identity in 5 residues overlap; Score: 23.0; Gap frequency: 0.0%

seq 131 VRAYW
seq 17 LRAHW
* * *

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Sequence Alignment and Identity Table **GenBank: AAG06957 and GenBank: AAA25891**

```

AAA25891      (1) MSVPVRHLIAGAFVEGLGAQRIPVSNPLDNSTLAEIACASAEQVEQAVAS
AAG06957      (1) -----
Consensus     (1)

                    1                               50

AAA25891      (51) ARETFASWKETPVSERARVMLRYQALLKEHHDELAKIVSSELGKTFEDAK
AAG06957      (1) -----
Consensus     (51)

                    51                               100

AAA25891      (101) GDVWRGIEVVEHACNVPSLLMGETVENVARNIDTYSITQPLGVCVGITPF
AAG06957      (1) -----
Consensus     (101)

                    101                              150

AAA25891      (151) NFPAMIPLWMFPLAIACGNAFILKPSEQVPLTSVRLAELFLEAGAPKIVL
AAG06957      (1) -----MTDIIFL
Consensus     (151) A L

                    151                              200

AAA25891      (201) QVHGGKEQVDLLKHPOVKAVSF GSVAVGQYVYHT T HNKRSQSFAG
AAG06957      (8)  GGNMGGPMAALLKAGHRVNVFD QPKAVLGLVEQG Q ADSAQCCQG
Consensus     (201) L G NLLK V L AV V A A LQ G

                    201                              250

AAA25891      (251) AKNHV PD DKAQV SNLVG S AA Q C AISV V VGAAREW PE
AAG06957      (58) AEVV S PA QHVES YLGDD L RV G P LIDC T APETARK AE
Consensus     (251) A I ILP A I A LA A K L I A I I E

                    251                              300

AAA25891      (301) IRDAL KVRPGP-----WDD GASYGPVINPQAKARIERL GCGEEG
AAG06957      (108) AAAAK LTLDPVSGGVGGAR GTLSFIVGGPAEGFARARP LEN GRN
Consensus     (301) A A AG V P R I M

                    301                              350

AAA25891      (344) AQLLLDGR YKVEGYPDGNW GPT F GVRPDMAIY EE FGPVLCLAEV
AAG06957      (158) IFHAGDHG GQVAKICNNML GIL A TAEALALGV NG DPAVLSEVMK
Consensus     (351) D A V LG L A K L VL

                    351                              400

AAA25891      (394) DSLEQAIRLINESP GNGTSIFT SG AARTFQHH EVGQ G N PIPVP
AAG06957      (208) QSSGNWALNLYNP PGVMPQAP SN YAGGFQVR MNKD G A ANAQA
Consensus     (401) S L PW AS A A FQ I LGI I

                    401                              450

AAA25891      (444) PFF FTGWK SFYGDHAY --K-QG RFY ETKTVT WFDSDSVAGT
AAG06957      (258) QAS PLGAL RNLFSLHAG DAEHEG DFS IQKLYR SD-----
Consensus     (451) L S G A LHA A GL F S K AK

                    451                              500

AAA25891      (491) NFSIQMR
AAG06957      (299) -----
Consensus     (501)

```

	AAA25891	AAG06957
AAA25891		14
AAG06957		

Sequence Alignment: alanine 2,3-aminomutase

				1	50
B. subtilis - SEQ. 22	(1)	MKNKWKYKPKRHWKEIELWKDVPEEWWDWQWOLTHVRTLDDLKVKVNL			
B. subtilis - SEQ. 24	(1)	MKNKWKYKPKRHWKEIELWKDVPEEWWDWQWOLTHVRTLDDLKVKVNL			
P. gingivalis - SEQ. 26	(1)	-----MAESRKYYPDVT EQWYDWHWQWLNRETLDDLQKKYTLT			
Consensus	(1)	MKNKWKYKPKRHWKEIELWKDVPEEKWNDWLWQLTHVRTLDDLKVKVNL		51	100
B. subtilis - SEQ. 22	(51)	EEEGVRLSKTIPLNITPYYSLMDPDNP CPVRMQSPVSEEMHKTK			
B. subtilis - SEQ. 24	(51)	EEEGVRLSKTIPLNITPYYSLMDPDNP CPVRMQSPVSEEMHKTK			
P. gingivalis - SEQ. 26	(43)	AEEEGVRLSPKVRMAITPYYSLSLMDPNPCPRKQPTQOEVIAL			
Consensus	(51)	EDEEGVRLSKTIPLNITPYYSLSLMDPDNP RCPVRMQSPVPLSEEMHKTK		101	150
B. subtilis - SEQ. 22	(101)	YDMEDPLHEDEDSVPVGLTHRYPDRVLFVLTNQCSYCRCTRRRF GQK			
B. subtilis - SEQ. 24	(101)	YDMEDPLHEDEDSVPVGLTHRYPDRVLFVLTNQCSYCRCTRRRF GQK			
P. gingivalis - SEQ. 26	(93)	EDQVDFPLSEDEDSVPVGLTHRYPDRVLFVLTQDKCSYCRCTRRRF GQK			
Consensus	(101)	YDMEDPLHEDEDSVPVGLTHRYPDRVLFVLTNQCSYCRHCTRRRFSGQI		151	200
B. subtilis - SEQ. 22	(151)	GMGVPPKQLDAAIAYIRETPETRDCLISGGDLLINDQILEYILKRLRSI			
B. subtilis - SEQ. 24	(151)	GMGVPPKQLDAAIAYIRETPETRDCLISGGDLLINDQILEYILKRLRSI			
P. gingivalis - SEQ. 26	(143)	DASSPSERDRCIDIYIANTPT RDVLISGGDLL SDERLEYILKRLREI			
Consensus	(151)	GMGVPPKQLDAAIAYIRETPETRDCLISGGDLLINDQILEYILKRLRSI		201	250
B. subtilis - SEQ. 22	(201)	PHLEVIRIGTRAPVVPQRITDHLCEILKKYHPVWLNTHFNFTSIEMTEES			
B. subtilis - SEQ. 24	(201)	PHLEVIRIGTRAPVVPQRITDHLCEILKKYHPVWLNTHFNFTSIEMTEES			
P. gingivalis - SEQ. 26	(193)	PHLEVIRIGTRAPVVPQRITDHLCEILKKYHPVWLNTHFNHNPNEFTSIEMTEES			
Consensus	(201)	PHLEVIRIGTRAPVVPQRITDHLCEILKKYHPVWLNTHFNFTSIEMTEES		251	300
B. subtilis - SEQ. 22	(251)	VEACEANAGPVGNOAVVLGINDSVPIMKKLMHDLVKIRVRPYYIYQ			
B. subtilis - SEQ. 24	(251)	VEACEANAGPVGNOAVVLGINDSVPIMKKLMHDLVKIRVRPYYIYQ			
P. gingivalis - SEQ. 26	(243)	VEACEANAGPVGNOAVVLGINDCTHIMKKLMHDLVKIRVRPYYIYQ			
Consensus	(251)	VEACEKLVNAGVPVGNOAVVLGINDSVPIMKKLMHDLVKIRVRPYYIYQ		301	350
B. subtilis - SEQ. 22	(301)	CDLSGIGHFRAPVSKGLEIIEGLRGHTSGYAVPTFVVHAPGGGGKIALQ			
B. subtilis - SEQ. 24	(301)	CDLSGIGHFRAPVSKGLEIIEGLRGHTSGYAVPTFVVHAPGGGGKIALQ			
P. gingivalis - SEQ. 26	(293)	CDLSGIGHFRTPVSKGLEIIEENLRGHTSGYAVPTFVVHAPGGGGKIPIT			
Consensus	(301)	CDLSEGIGHFRAPVSKGLEIIEGLRGHTSGYAVPTFVVHAPGGGGKIALQ		351	400
B. subtilis - SEQ. 22	(351)	PNYVLSQSPDKVILRN EGVITSYPEPENYIPNOADAYFESVFPETADKK			
B. subtilis - SEQ. 24	(351)	PNYVLSQSPDKVILRN EGVITSYPEPENYIPNOADAYFESVFPETADKK			
P. gingivalis - SEQ. 26	(343)	PNYVLSQSPRHVILRN EGVITSYPEPE-----NYEECDCEPCRAGK			
Consensus	(351)	PNYVLSQSPDKVILRN EGVITSYPEPENYIPNOADAYFESVFPETADKK		401	450
B. subtilis - SEQ. 22	(401)	EPIGLSAIFADKEVSFTPENVDRIKREAYIANPEHETLKDRREKRDQLK			
B. subtilis - SEQ. 24	(401)	EPIGLSAIFADKEVSFTPENVDRIKREAYIANPEHETLKDRREKRDQLK			
P. gingivalis - SEQ. 26	(386)	HKEGSAISGOQIEPSDARKKR--DKN-----			
Consensus	(401)	EPIGLSAIFADKEVSFTPENVDRIKREAYIANPEHETLKDRREKRDQLK		451	471
B. subtilis - SEQ. 22	(451)	EKKFLAQKKQKETECGGDSS			
B. subtilis - SEQ. 24	(451)	EKKFLAQKKQKETECGGDSS			
P. gingivalis - SEQ. 26	(417)	-----			
Consensus	(451)	EKKFLAQKKQKETECGGDSS			

	B. subtilis – SEQ. 22	B. subtilis – SEQ. 24	P. gingivalls – SEQ. 26
B. subtilis – SEQ. 22		100	59
B. subtilis – SEQ. 24			59
P. gingivalis – SEQ. 26			